

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/538,038A  
Source: FWO  
Date Processed by STIC: 6/20/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/538,038A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3   J   Misaligned Amino  
    Numbering             The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII             The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length       Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"                 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)         Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)         SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi)        SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)         Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)         Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>  
    Response             Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11      Use of <220>         Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."  
                          Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12      PatentIn 2.0  
    "bug"                 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa       "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006  
TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT  
Output Set: N:\CRF4\06202006\J538038A.raw

2 <110> APPLICANT: Givaudan SA  
W--> 3 <120> TITLE OF INVENTION: G-Proteins  
W--> 4 <130> FILE REFERENCE: 30069PCT  
W--> 5 <140> CURRENT APPLICATION NUMBER: US 10/538,038A  
C--> 6 <141> CURRENT FILING DATE: 2005-06-08  
7 <150> PRIOR APPLICATION NUMBER: US 60/434,790  
8 <151> PRIOR FILING DATE: 2002-12-18  
W--> 9 <160> NUMBER OF SEQ ID: 2

## ERRORED SEQUENCES

W--> 10 <210> SEQ ID NO: 1  
11 <211> LENGTH: 1122 <212> DNA  
12 <213> ORGANISM: Homo sapiens  
W--> 13 <220> FEATURE:  
14 <221> NAME/KEY: CDS  
15 <222> LOCATION: (1)..(1122)  
16 <223> OTHER INFORMATION:

~~E--> 17 <212> TYPE: ignore this~~

W--> 17 <400> SEQUENCE: 1

18 atggcccgcgt cgcgtgacctg gcgcgtgctgc ccctggtgcc tgacggagga tgagaaggcc 60  
19 gccgcccggg tggaccagga gatcaacagg atcctcttg agcagaagaa gcaggaccgc 120  
20 ggggagctga agctgctgct tttgggcccc ggcgagagcg ggaagagcac cttcatcaag 180  
21 cagatgcgga tcatccacgg cgcgcggtac tcggaggagg agcgcaaggg cttccggccc 240  
22 ctggtctacc agaacatctt cgtgtccatg cgggccatga tcgaggccat ggagcggctg 300  
23 cagattccat tcagcaggcc cgagagcaag caccacgcta gcctggtcat gagccaggac 360  
24 ccctataaag tgaccacgtt tgagaagcgc tacgtgcgg ccattgcagt gctgtggagg 420  
25 gatgcgggca tccgggcctg ctatgagcgt cggcggggaat tccacctgct cgattcagcc 480  
26 gtgtactacc tgtcccacct ggagcgcac accgaggagg gctacgtccc cacagctcag 540  
27 gacgtgctcc gcagccgcat gccaccact ggcacaaag agtactgctt ctccgtgcag 600  
28 aaaaccaacc tgcggatcgt ggacgtcggg ggccagaagt cagagcgtaa gaaatggatc 660  
29 cattgtttcg agaactgat cgccctcatc tacctggcct cactgagtga atacgaccag 720  
30 tgcttgaggg agaacaacca ggagaaccgc atgaaggaga gcctcgcat gtttgggact 780  
31 atcctggaac taccttggtt caaaagcaca tccgtcatcc tctttctcaa caaaaccgac 840  
32 atcctggagg agaaaatccc cacctccac ctggctacct atttccccag tttccagggc 900  
33 cctaagcagg atgctgaggc agccaagagg ttcactctgg acatgtacac gaggatgtac 960  
34 accgggtgcg tggacggccc cgagggcagc aacttaaaaa aagaagataa ggaaatctat 1020  
35 tctcatatga cctgcgctac tgacacacaa aacgtcaaat tcgtgtttga tgccgtgaca 1080  
36 gatataataa taaaagagaa cctcaaagac tgtgggctct tc 1122

38 <210> SEQ ID NO: 2

39 <211> LENGTH: 374

40 <212> TYPE: PRT

? (see p.3 - the last-numbered amend and states "390")

Does Not Comply  
Corrected Diskette Needed

## RAW SEQUENCE LISTING

DATE: 06/20/2006

PATENT APPLICATION: US/10/538,038A

TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

41 <213> ORGANISM: Homo sapiens

W--> 42 <400> SEQUENCE: 2

43 Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu 1

E--> 44                   5       10       15 10       15

46 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu

E--> 47       20 20       25       25 30       30

49 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu

E--> 50       35       40       45

52 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile

E--> 53       50 55       60

55 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro

E--> 56 65       70       75       80

58 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala

E--> 59                   85       90       95

61 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His

E--> 62       100       105       110

64 Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu

E--> 65       115       120       125

67 Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile

E--> 68       130       135       140

70 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala

E--> 71 145       150       155       160

74 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val

E--> 75       165       170       175

77 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile

E--> 78       180       185       190

80 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp

E--> 81       195       200       205

83 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu

E--> 84       210 215       220

86 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln

E--> 87 225       230       235       240

89 Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala

E--> 90       245       250       255

92 Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val

E--> 93       260       265       270

95 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr

E--> 96       275       280       285

98 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp

E--> 99       290       295       300

101 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr

E--> 102 305       310       315       320

104 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Leu Lys Lys Glu Asp

E--> 105       325       330       335

107 Lys Glu Ile Tyr Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val

E--> 108       340       345       350

110 Lys Phe Val Phe Asp Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu

E--> 111       355       360       365

113 Lys Asp Cys Gly Leu Phe Ser His Leu Ala Thr Tyr Phe Pro Ser

*delete**misaligned**amino acid  
number**(see item 3**on Error**Summary**Sheet 1)**Invalid amino acid designator*

## RAW SEQUENCE LISTING

DATE: 06/20/2006

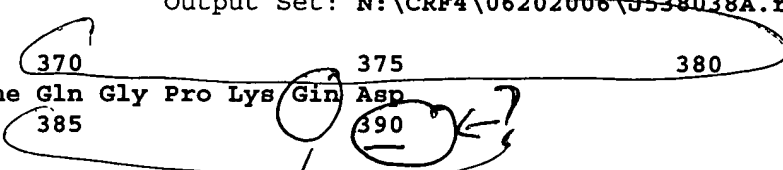
PATENT APPLICATION: US/10/538,038A

TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

E--> 114 370 375 380  
E--> 116 Phe Gln Gly Pro Lys Gln Asp  
E--> 117 385 390



*invalid amino acid designator*

**VERIFICATION SUMMARY**

DATE: 06/20/2006

PATENT APPLICATION: US/10/538,038A

TIME: 15:28:32

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:283 W: Missing Blank Line separator, <140> field identifier  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:283 W: Missing Blank Line separator, <160> field identifier  
L:10 M:283 W: Missing Blank Line separator, <210> field identifier  
L:13 M:283 W: Missing Blank Line separator, <220> field identifier  
L:17 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:17 M:283 W: Missing Blank Line separator, <400> field identifier  
L:17 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16  
L:42 M:283 W: Missing Blank Line separator, <400> field identifier  
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:98 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:116 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1